

SEQUENCE LISTING

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<120> Novel cytochrome P450 monooxygenases and their use for the oxidation of organic substrates

<130> 50915

<140> 10/031,146

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<151> 2000-07-27

<160> 9

<170> Word Perfect version 6.1

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 <211> 30  
 <212> DNA  
 <213> Synthetic sequence

<220>  
 <221> unsure  
 <222> 1..30  
 <223> n is g, a, t or c.

<220>  
 <223> Description of the synthetic sequence: PCR primer

<400> 3

gcaggagacg gggtgnnnac aagctggacg

30

<210> 4  
 <211> 30  
 <212> DNA  
 <213> Synthetic sequence

<220>  
 <221> unsure  
 <222> 1..30  
 <223> n is g, a, t or c.

<223> Description of the synthetic sequence: PCR primer

<400> 4

10

cgtccagctt gttnncaacc cgtctcctgc

30

<210> 5  
<211> 34  
<212> DNA  
<213> Synthetic sequence

<220>  
<221> unsure  
<222> 1..34  
<223> n is g, a, t or c.

&lt;223&gt; Description of the synthetic sequence: PCR primer

<400> 5  
gaagcaatga acaagnnnca gcgagcaaatt ccag

34

<210> 6  
<211> 30  
<212> DNA  
<213> Synthetic sequence

<220>  
<221> unsure  
<222> 1..30  
<223> n is g, a, t or c.

&lt;223&gt; Description of the synthetic sequence: PCR primer

<400> 6  
ctggatttgc tcgctgnnnc ttgttcattg

30

<210> 7  
<211> 41  
<212> DNA  
<213> Synthetic sequence

<220>  
<221> unsure  
<222> 1..41  
<223> n is g, a, t or c.

&lt;223&gt; Description of the synthetic sequence: PCR primer

&lt;400&gt; 7

gctttgataa aaacttaaag tcaannnctt aaatttgtac g

41

<210> 8  
<211> 40  
<212> DNA  
<213> Synthetic sequence

<220>  
<221> unsure  
<222> 1..40  
<223> n is g, a, t or c.

&lt;223&gt; Description of the synthetic sequence: PCR primer

cgtacaaatt taagnnnttg acttaagttt ttatcaaagc

<211> 1049

<212> PRT

<213> Bacillus megaterium

<400> 9

Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys  
20 25 30

Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg  
35 40 45

Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp  
50 55 60

Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg  
65 70 75 80

Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn  
85 90 95

Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala  
100 105 110

Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val  
115 120 125

Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu  
130 135 140

Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn  
145 150 155 160

Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr  
165 170 175

Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala  
180 185 190

Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu  
195 200 205

Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg  
210 215 220

Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn  
225 230 235 240

Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg  
245 250 255

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Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly  
 260 265 270  
 Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu  
 275 280 285  
 Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro  
 290 295 300  
 Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn  
 305 310 315 320  
 Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala  
 325 330 335  
 Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp  
 340 345 350  
 Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp  
 355 360 365  
 Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser  
 370 375 380  
 Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala  
 385 390 395 400  
 Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly  
 405 410 415  
 Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu  
 420 425 430  
 Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys  
 435 440 445  
 Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr  
 450 455 460  
 Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn  
 465 470 475 480  
 Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly  
 485 490 495  
 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro  
 500 505 510  
 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly  
 515 520 525  
 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn  
 530 535 540  
 Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val  
 545 550 555 560  
 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala  
 565 570 575

Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala  
 580 585 590  
 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp  
 595 600 605  
 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp  
 610 615 620  
 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys  
 625 630 635 640  
 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu  
 645 650 655  
 Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu  
 660 665 670  
 Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu  
 675 680 685  
 Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile  
 690 695 700  
 Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly  
 705 710 715 720  
 Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu  
 725 730 735  
 Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln  
 740 745 750  
 Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met  
 755 760 765  
 Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu  
 770 775 780  
 Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr  
 785 790 795 800  
 Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser  
 805 810 815  
 Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile  
 820 825 830  
 Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser  
 835 840 845  
 Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile  
 850 855 860  
 Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys  
 865 870 875 880  
 Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu

14

	885		890		895
Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg					
	900		905		910
Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu					
	915		920		925
Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr					
	930		935		940
Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr					
	945		950		955
Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val					
	965		970		975
Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp					
	980		985		990
Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro					
	995		1000		1005
Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val					
	1010		1015		1020
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly					
	1025		1030		1035
Arg Tyr Ala Lys Asp Val Trp Ala Gly					
	1045				